



<110> Ruan, Yong-Ling
Furbank, Robert T.
Danny, Llewellyn J.

<120> Modification of sucrose synthase gene expression in plant tissue and
uses therefor

<130> GHSUSY W01

<150> 60/251852

<151> 2000-12-08

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 2625

<212> DNA

<213> Gossypium hirsutum

<220>

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gat gag acc ctt ctt gct cac agg aac gag att ttg gcc ttg ctc tca	96
Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser	
20 25 30	
agg atc gag ggc aaa gga aaa gga att ctg caa cac cat caa att att	144
Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile	
35 40 45	
cta gag ttt gaa gct atc cct gaa gag aac aga aag aag ctc gct aat	192
Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn	
50 55 60	
ggg gca ttt ttt gaa gta ttg aag gct agt cag gaa gcg atc gtg ttg	240
Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu	
65 70 75 80	

cct cca tgg gtt gca ctt gct gtt cgt cca agg cct ggt gtt tgg gag Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu	288
85 90 95	
tac att aga gtg aat gtt cac gcc ctt gtt gtt gag gaa ctc act gtt Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val	336
100 105 110	
gct gag tat ctc cac ttc aag gaa gag ctt gtt gat gga agt tca aat Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn	384
115 120 125	
gga aac ttt gtt ttg gaa ttg gat ttt gag ccc ttc aac tca tca ttc Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe	432
130 135 140	
ccc cgc cca act ctt tca aaa tcc att ggt aat ggt gtg gag ttc cta Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu	480
145 150 155 160	
aat cgt cac ctt tgc gca aaa ttg ttc cat gac aag gag agc atg cac Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His	528
165 170 175	
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180 185 190	
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195 200 205	
agg aaa gca gag gag tat ctt ggt acc cta cct cct gag aca cca tgt Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys	672
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gcc gaa ttc gaa cac cgg ttc cag gaa atc ggt ttg gaa aga ggt tgg Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp	720
225 230 235 240	
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245 250 255	
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260 265 270	
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275 280 285	

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aga ctt ctt cct gat gct gtc gga aca aca tgc ggt caa cga ctt gag Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu 340 345 350	1056
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tgg cca tac ttg gaa acc tac aca gag gat gtt gct cat gaa atc tcc Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser 385 390 395 400	1200
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tgc acc atc gcc cat gct ttg gag aag aca aaa tat cca gat tca gat Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp 435 440 445	1344
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aca gct gat ctt ttt gca atg aac cat aca gat ttc atc atc acc agt Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser 465 470 475 480	1440
act ttc cag gaa att gca gga agc aag gac act gtt ggt caa tac gag Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu 485 490 495	1488

agc cac act gct ttc act ctt cct ggt ctc tac cgt gtt gta cat ggt Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly 500 505 510	1536
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gaa cac tta tgt gtg ctc aat gac cgc aac aag cca att ctg ttc aca Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr 565 570 575	1728
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ggg ggt gat agg cga aag gaa tct aaa gat ttg gaa gag aag gct gaa Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu 610 615 620	1872
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ttc aga tgg ata tca tct caa atg aac aga atc cga aat gtt gaa ctt Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu 645 650 655	1968
tac cga tac att tgc gac acg aaa ggt gcc ttt gta cag cct gca ttg Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu 660 665 670	2016
tat gaa gcc ttt gga ttg aca gtt gtg gag gca atg act tgc ggt ttg Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu 675 680 685	2064
cca aca ttc gca acc tgt aac ggt gga cca gcc gag att att gtc cat Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His 690 695 700	2112

ggg aaa tct ggt ttc aac att gat cct tac cat ggt gat caa gct gct 2160
 Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala
 705 710 715 720
 gac ata ctc gtc gat ttc ttt gaa aag tgt aag aaa gat cca tct cac 2208
 Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His
 725 730 735
 tgg gat aag atc tcc caa gga ggc ttg aaa cga ata gag gag aag tat 2256
 Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr
 740 745 750
 aca tgg aag att tac tgc gag aga cta ttg acc ctg aca gga gtg tat 2304
 Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr
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 Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg
 770 775 780
 tac ctt gag atg ttt tat gct ctt aag tac cgt aag ctg gct gaa tca 2400
 Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser
 785 790 795 800
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 Val Pro Leu Ala Glu Glu Ile Glu Pro Val Lys His Trp Ala
 805 810
 ggt ttt tct tgg aga ata ata ttc tgt ttt gta att tca att gga gaa 2496
 Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser Ile Gly Glu
 815 820 825 830
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 Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe Phe Ala Gly
 835 840 845
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 Ile Val Thr Trp Gly Cys Ala Pro Val Asn Ser Ser Ile Trp
 850 855 860
 tga ctt ttg ttt ttc aaa aaa aaa aaa aaa aaa 2625
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<212> PRT

<213> Gossypium hirsutum

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<222> (414)..(414)

<223> The 'Xaa' at location 414 stands for Asn, Asp, His, or Tyr.

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Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile
35          40          45

Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn
50          55          60

Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
65          70          75          80

Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
85          90          95

Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
100         105         110

Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn
115         120         125

Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe
130         135         140

Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
145         150         155         160

Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His
165         170         175

Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met
180         185         190

Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu
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Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys
210         215         220

Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225         230         235         240

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Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
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 Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe
 275 280 285
 Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
 290 295 300
 Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg
 305 310 315 320
 Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr
 325 330 335
 Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu
 340 345 350
 Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg
 355 360 365
 Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val
 370 375 380
 Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser
 385 390 395 400
 Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp
 405 410 415
 Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln
 420 425 430
 Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp
 435 440 445
 Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe
 450 455 460
 Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser
 465 470 475 480
 Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu
 485 490 495
 Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly
 500 505 510

Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp
 515 520 525
 Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His
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 Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu
 545 550 555 560
 Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr
 565 570 575
 Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp
 580 585 590
 Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val
 595 600 605
 Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu
 610 615 620
 Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln
 625 630 635 640
 Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu
 645 650 655
 Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu
 660 665 670
 Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu
 675 680 685
 Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His
 690 695 700
 Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala
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 Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His
 725 730 735
 Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr
 740 745 750
 Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr
 755 760 765
 Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg
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 Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser
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Val Pro Leu Ala Glu Glu
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<212> PRT
<213> Gossypium hirsutum

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Phe Ala Gly Ile Val
35

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<213> Gossypium hirsutum

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